On page 16 please replace the paragraph beginning at line 3 with the following paragraph.

--(b) in other adenoviruses the E4 region is normally located at the right-hand end of the genome. the OAV287 E4? region is tentatively identified based only on the presence of a protein sequence motif HCHC ... PGSLQC (SEQ ID NO. 4) which is found in 18.8 kD and 30.85 kD orfs in this region. Identical or very similar motifs are found in the E4 34 kD protein of human Ad2 and Ad40 and mouse adenoviruses;–

On page 17 please replace the paragraph bridging page 18 with the folloing paragraph.

--The circular genome clone differs from the naturally occurring circles that occur in Ad5-infected cells (10) and that might exist in OVA2887-infected cells in that the] 46 base pair ITRs are joined by a GATC linker. Together with the last and first nucleotides of the genome (G and C, respectively, see Figure 1), this sequence forms a unique KpnI site when the ITRs are joined head to tail. Other sites such as EcoRI, BamHI, SalI, KasI, etc. which have recognition sequences beginning with G and ending with Care suitable if they are uniqueas the 3' and 5' terminal nucleotides of other adenovirus genomes are G and C, respectively. A plasmid with a sutable antibiotics resistance gene e.g. amp^R and origin of replication can be inserted at the unique site or elsewhere in the genome to form a plasmid which can be propagated in bacteria. Plasmids propagated in the presence of 200 µg/ml ampicillin in *E. coli* strains JM109 and DH5-alpha retain the KpnI sites and ins rted sequ nces, indicating that the OAV287 ITR sequences are stable when linked in this manner. This approach may therefore b used to